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J. Biol. [5]

SEQUENCE OF 550-572 FROM N.A. MEDLINE-86033917; PubMed-3902830;

MEDLINE-89308683; PubMed=2663858; Grabau C., Chang Y.Y., Cronan J.E. Jr.; Third binding by Escherichia coli pyruvate oxidase is disrupted small alterations of the carboxyl-terminal region."; J. Biol. Chem. 264:12510-12519(1989).

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Mol. Microbiol. 11:1019-1028(1994).
-i- CATALYTIC ACTIVITY: PYRUVATE + FERRICYTOCHROME B1 +
+ ACETATE + FERROCYTOCHROME B1.
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                                                                                                                                                                                                                                                                                                                             MUTAGEN
                                                                                                                                                                                                                                                                                                                                            ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                      PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [NTERPRO;
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SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED.

PTM: ACTIVATED BY LIMITED PROTEOLYTIC DIGESTION. THIS CLEAVAGE PRODUCES A DEPTIDE (ALPHA-PEPTIDE) AND MIMICS THE ACTIVATION OF ENZYME BY PHOSPHOLIPIDS. THE PROTEOLYTIC CLEAVAGE ALSO RESULTS THE LOSS OF THE HIGH AFFINITY LIPID-BINDING SITE OF THE ENZYME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     L; X04105; CAA27725.1; -.
L; AE000188; AAC73958.1; -.
D90724; BAA35585.1; -.
L; S73268; AAB31180.1; -.
L; M28208; AAB59101.1; -.
L; L47688; AAB59102.1; -.
L; L47689; AAB59104.1; -.
L; L47691; AAB59104.1; -.
L; L47691; AAB59105.1; -.
L; L47692; AAB59107.1; -.
L; L47693; AAB59107.1; -.
L; L47694; AAB59107.1; -.
L; L47695; AAB59108.1; -.
L726428; AAB59108; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COFACTOR: THIAMINE PYROPHOSPHATE, FAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A23648; DEECPC.
266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PF00205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E; G058.0; 6TH
EG10754; POXB
                                                                                                                                                                                                                                                                                                                                                                                                                                  PS00187;
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Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                             TPP_enzymes; 1.
87; TPP_ENZYMES;
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                                                                                               ALPHA-PEPTIDE.
BY SIMILARITY.
A-YT: IN POXB11.
A-YV: IN POXB14.
D-PP: IN POXB15; NORMAL ACTIVITY.
E-PP: IN POXB16; LOSS OF ACTIVITY.
R->G: IN POXB16; REDUCED ACITIVITY; MISTACT LESS WITH MEMBRANES.
MISSING: IN POXB6.
MISSING: IN POXB6.
MISSING: IN POXB6.
MISSING: IN POXB6.
OD -> HE (IN REF. 4).
OQ AL -> HGV (IN REF. 4).
OAL -> HGV (IN REF. 4).
OAL -> HGV (IN REF. 4).
                   Score 1317.5; DB 1; Pred. No. 3.7e-79;
                                                                                                                                                                                                                                                                                                                                                                                                              FAD;
    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                            Thiamine
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  HSSP; P3/000, IPR000399; ...
INTERPRO; IPR000399; ...
PRAM; PF00205; TPP_enzymes; PRAM; PF00205 and Protein.
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01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
01-NOV-1990 (Rel. 16, Last annotation update)
HYPOTHETICAL 42.6 KDA PROTEIN IN ISOAMYLASE 3'REGION.
                                                                                                                                                                                                                                                                                            use
                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=SB-15; Amemura A., Fujita M., Futai M.; Submitted (NOV-1988) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: SIMILAR TO E.COLI ACETOHYDROXY ACID SYNTHASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pseudomonas amyloderamosa.
Bacteria; Proteobacteria.
                                                                                                                               PIR;
                                                                                                                                                  EMBL;
                                                                                                                                                                                                         entities requires a license agreement (S or send an email to license@isb-sib.ch).
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Hypothetical SEQUENCE 39
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                                                                                                                                                                                                                                                                 ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way lifted and this statement is not removed. Usage by and for commercial
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396 AA; 4
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Best Local S
Matches 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-AAL-1 / DSM 2661 / ATCC 43067:

STRAIN-BAL-1 / DSM 2661 / ATCC 43067:

MEDLINE-96337999; PubMed-8688087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 35, Last annotation update)
PROBABLE ACETOLACTATE SYNTHASE LARGE SUBUNIT (EC 4.1.3.18)
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057725;
01-NOV-1997
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the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                           "Complete genome sequence of jannaschii."; Science 273:1058-1073(1996).
                                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entry of 
                                                                                                                                                                                                                                                                                                                                                                                                                             Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M., Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.; "Complete genome sequence of the methanogenic archaeon, Methanoco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Methanococcus jannaschii
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                                                                                                                                                                                                             PATHWAY: FIRST STEP IN VALINE AND ISOLEUCINE BIOSYNTHESIS SUBUNIT: DIMER OF LARGE AND SMALL CHAINS (BY SIMILARITY). SIMILARITY: WITH OTHER ENZYMES WHICH REQUIRE TPP.
                                                                                                                                                                                                                                                                                                                      CATALYTIC ACTIVITY: 2-ACETOLACTATE COFACTOR: THIAMINE PYROPHOSPHATE, I
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Pred. No. 3.0
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Best Local :
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                                                                 01-JUN-1994 (Rel. 29, Created)
01-OCT-1994 (Rel. 30, Last sequence up
01-FEB-1995 (Rel. 31, Last annotation
PYRUVATE OXIDASE (EC 1.2.3.3) (PYRUVIC
Lactobacillus plantarum.
Bacteria; Firmicutes; Bacillus/Clostrl
MEDLINE-94194507; PubMed-8145244.
Muller Y.A., Schumacher G., Rudol
                                                                                                                                                                      LACPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
HSSP;
TIGR;
                                                                                                                                             POXB_LACPL P37063;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thiamine pyrophosphate; Lyase. ACT_SITE 47 47 ESEQUENCE 591 AA; 64492 MW;
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PROSTTE; PS00187; TPP_ENZYMES; 1.
Branched-chain amino acid biosynthesis;
                                                         Lactobacillus.
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P06169; 1YPD.
MJ0277; -.
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29.5%;
                                                                  Bacillus/Clostridium
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       Rudolph
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, DB398C926D9B3A9D CRC64;
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                                                                                           notation update)
(PYRUVIC OXIDASE)
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                                                                  group;
        G.E.;
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SCIENCE 259:965-967(1993).

FUNCTION: IMPORTANT FOR THE AEROBIC GROWTH. DECARBOXYLATES PYROVATE IN FOUR STEPS. THE ENERGY RELEASED IS PARTIALLY STOR IN ACETYL PHOSPHATE.

FUNCTION CONTAINS A SIX-STRANDED PARALLEL BETA SHEET SURROUNDED BY ALP CONTAINS A SIX-STRANDED PARALLEL BETA SHEET SURROUNDED BY ALP CONTAINS.
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PROSITE: PS00187; TPP_ENZYMES;
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SIMILARITY: WITH OTHER ENZYMES WHICH REQUIRE TPP.
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Wipat A., Carter N., Brignell C.S., Guy J.B., Piper K.,
Sanders J., Emmerson P.T., Harwood C.R.;
"The dnaB-pheA (256 degrees-240 degrees) region of the Bacillus subtills chromosome containing genes responsible for stress responses, the utilization of plant cell walls and primary metabolism.";
                                                                                                                                                                                                                    STRAIN-IS58;
STRAIN-97443988; PubMed-9298659;
MEDLINE-97443988; PubMed-9298659;
                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-20 FROM N.A. MEDLINE-92250415; PubMed=1577690; Grandoni J.A., Zahler S.A., Calvo J "Transcriptional regulation of the subtilis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ILVB_BACSU STANDARD; PRT; 573 AA. p37251; p94564; 01-OCT-1994 (Rel. 30, Created) 30-MAY-2000 (Rel. 39, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) ACETOLACTATE SYNTHASE LARGE SUBUNIT (EC 4.1.3.18) (AHAS) (ACETOHYDROXY-ACID SYNTHASE LARGE SUBUNIT) (ALS) (VEGETATIVE)
                                                                                                        Bactillus subtilis.
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Zahler S.A.;
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                  modified and
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                                                                                                                                                                                                                                                                                                                                                                                               Microbiology 142:3067-3078(1996).
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               s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss institute of Bioinformatics and the EMBL outstation - European Bioinformatics institute. There are no restrictions on the by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial
                                                                                             SIMILARITY: WITH OTHER ENZYMES WHICH REQUIRE TPP.
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KW Branched-chain amino acid biosynthesis; Fl

W Thlamline pyrophosphate; Lyase.

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CONFLICT 79 88 KPGVVIATSG ->

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                                                                                                                   GUITH
                                                                                                                                                                                               EMLVEGQPEFGTDHEEVNFAEIAAAAGIKSVRITDPKKVREQLAEALAYPGPVLIDI
                                                                                                                                                                                                                                   GLPAAIGAQLAEKDATVVAVVGDGGFQMTLQELDVIRELNLPVKVVILNNACLGMVRQWQ
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                        18 (Rel. 37, List sequence upd. 38 (Rel. 37, Last sequence upd. 99 (Rel. 38, Last annotation u 97 (Rel. 38) LARGE SUBUNIT (EC )ROXY-ACID SYNTHASE LARGE SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR000399;
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                                                                                                                   STANDARD;
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A -> R (IN REF. 1).
NSGLVHILP -> IQVGTYPS (IN KPGYVIATSG -> NRCRICHVR (
KPGYVIATSG -> NRCRICHVR (
E2D536847A2B0CA7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 554.5; DB 1;
Pred. No. 3.8e-29;
3; Mismatches 251;
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Flavoprotein;
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Chloroplast Guillardia

theta

(Cryptomonas

(ACETOHYDROXY-ACID

SUBUNIT) (ALS). on update) (EC 4.1.3.18)

(AHAS)

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Duery Match
Best Local
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PROSITE; PS00187; TPP_ENZYMES; 1.
Branched-chain amino acid biosynthesis; Flavoprotein; Thiamine pyrophosphate; Lyase; Chloroplast.
ACT_SITE 60 60 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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"The plastid genome of the cryptophyte alga, Guillar complete sequence and conserved synteny groups confi ancestry with red algae.";
J. MOI. EVOI. 48:236-244(1999).
-i- CATALYTIC ACTIVITY: 2-ACETOLACTATE + CO(2) = 2-P-1- CATALYTIC ACTIVITY: 3-ACETOLACTATE, AND MAGNESIUM
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PFAM; PF00205;
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Local Similarity 28.0%;
hes 161; Conservative 11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ELAVCAASCGPGNTHLIQGLYDSHRNGAKVLAIASHIPSAQIGSTFFQE-----THPEI 118 : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
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                                                     NNSSLGMVK-LEMLVEGQPEFGTDHEE--VNFAEIAAAAGIKSVRITDPKKVREQLAEAL
                                                                                                             WITSAGLGTMGYGLPAAIGVQIAHPNEQVICISGDASFQMNIQELGTVSQYGLPIKIFII
                                                                                                                                                                                                                              WRKEYPLLVPKNINNLSPQ---EVIHEISTEATNAYFTTDVGQHQMWAAQFIKTSQ--KR
                                                                                                                                                                                                                                                                                VVETYTHNVEKHV-PIHPEYVASILNELADK--DAVFTVDTGMCNVWHARYIENPEGTRD
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{\tt NNKWQGMVRQWQQAFYGERYSHSNMEKGAPNFTKVAEAFGLRSLKIKSRNDLKLRIKEAL}
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Pred. No. 9.1e
14; Mismatches
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Query Match
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Matches 161
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EMBL; M94625; AAA03052.
PIR; S27402; S27402.
PIR; S28920; S28920.
HSSP; P06109; IYPD.
INTERPRO; IPR000399; -.
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01-JUL-1993
01-OCT-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Complete nucleotide genome.";
Plant Mol. Biol. Rep.
                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACETOLACTATE
                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=93153832; PubMed=8381336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPECIES=P.UMBILICALIS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Reith M., Munholland J.M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PATHWAY: FIRST STEP IN VALINE AND ISOLEUCINE BIOSYNTHESIS SUBUNIT: DIMER OF LARGE AND SMALL CHAINS (BY SIMILARITY).
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LLDSIVRHGVIHIFGYPGGAILPIYDELYAWEELSLIKNILVRHEQGASHAADAYSRSTG
                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Rel. 26, Created)
(Rel. 26, Last sequence update)
(Rel. 34, Last annotation update)
SYNTHASE LARGE SUBUNIT (EC 4.1.3)
Y-ACID SYNTHASE LARGE SUBUNIT) (AI
                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                           AAC08216.1;
AAA03052.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bangiales; Bangiaceae; Porphyra
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WEDLINE-98295987; PubMcd-9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
Dadcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Davles R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
Davles R., Devlin K., Krogh A., McLean J., Moule S., Murphy L.,
A Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
A Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
A Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
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A Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
A Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
A Hutter S., Seeger K., Skelton S., Squares S., Sgares R., Sulston J.E.
A Taylor K., Whitehead S., Barrell B.G.;
Technology of Mycobacterium tuberculosis from the Complete genome sequence.";
The Complete genome sequence.";
L. Lature 393:537-544(1998).
L. Lature 393:537-544(1998).
L. Lature 393:537-544(1998).
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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30-MAY-2000
30-MAY-2000
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                                                                                                                                     PATHWAY: FIRST
SIMILARITY: WIT
                                  European Bioinformatics Institute.
                                                                                                                                                                                              SIMILARITY)
                                                   SWISS-PROT entry is copyright. It is produced through a collaboratic en the Swiss Institute of Bioinformatics and the EMBL outstation
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Branched-chain amino acid biosynthesis;
Thiamine pyrophosphate; Lyase.
ACT_SITE 84 84 BY SIMILARI;
SEQUENCE 618 AA; 66122 MW.
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                                    Escherichia
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01-AUG-1988 (Rel. 08, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
ACETOLACTATE SYNTHASE ISOZYME I LARGE SUBUNIT
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                  Proteobacteria;
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SEQUENCE FROM N.A.
MEDLINE=85242084; P
Wek R.C., Hausser C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=85242084; PubMed=2989782; Wek R.C., Hausser C.A., Hatfield G.W.; The nucleotide sequence of the ilvBN operon of Escherichia sequence homologies of the acetohydroxy acid synthase isozyn Nucleic Acids Res. 13:3995-4010(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; J01633; AAA24017.1; -. EMBL; X02541; CAA26387.1; -. EMBL; L10328; AAA62023.1; -.
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"The ilvB locus of Escherichia coli K-12 is
subunits of acetohydroxyacid synthase I.";
Nucleic Acids Res. 13:3979-3993(1985).
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the European Bioinformatics Institute.
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ACT_SITE 60 60 E
SEQUENCE 562 AA; 60440 MW;
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PFAM; PF00205; TPP_ENZYMES; 1.

PROSITE; PS00109; TPP_ENZYMES; 1.

Branched-chain amino acid biosynthesis; Flavoprotein; Magnesium;
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SWISS-2DPAGE; P08142; COLI
ECO2DBASE; D057.0; 6TH EDI7
ECOGENE; EG10494; ILVB.
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SIMILARITY: WITH OTHER ENZYMES WHICH REQUIRE TPP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is the Swiss Institute of Bioinformatics and uncertainty is copyright. It is the Swiss Institute of Bioinformatics and uncertainty is a long as its content and the swiss is content.
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                                                              GYCEMVNGGEQGERILHHAIQSTMAGK-GVSVVVIPGDI--
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                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute.
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                                                               Thiamine
                                                                                   Branched-chain amino acid
                                                                                                         PROSITE;
                                                                                                                               PFAM; PF00205;
                                                                                                                                                                      HSSP;
                                                                                                                                                                                                            EMBL; M75907; AAA26595.1;
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                                                           pyrophosphate.
                                                                                                           PS00187;
                                                                                                                                                                                                                                                                                                                                                             the Swiss Institute of Bioinformatics
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Cyanobacteria;
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E SYNTHASE
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si E., Zanaria E.,
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MBL outstation -
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SEQUENCE FROM N.A.
STRAILNEH12 / MG1655;
MEDLINE-92358234; PubMed-1379743;
Daniels D.L., Plunkett G. III, Bu.
                                                                                                                                                                                                                                                                                                                     P00892: p76749;
21-JUL-1986 (Rel. 01, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
ACETOLACTATE SYNTHASE ISOZYME II LARGE SUBUNIT (EC 4.1.3.18)
(ACETOHYDROXY-ACID SYNTHASE II LARGE SUBUNIT) (ALS-II).
                                                                                        "The complete nucleotide sequence Escherichia coli K-12."; Nucleic Acids Res. 15:2137-2155(19)
                                                                                                                                                                                                      STRAIN-K12
                                                                                                                                                                                                                   SEQUENCE FROM
                                                                                                                                              Hatfield G.W.;
                                                                                                                                                               Lawther R.P.,
                                                                                                                                                                                   MEDLINE-87174741;
                                                                                                                                                                                                                                                                          Bacteria;
                                                                                                                                                                                                                                                                                         Escherichia coli
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                                                                                                                                                                                                                                                                      Proteobacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                               PubMed=3550695;
R.C., Lopes J.M.,
                                                                                        15:2137-2155(1987)
                                                                                                                                                                                                                   AND
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27.8%;
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Pred.
   Burland V.D.,
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 R EMBL; X04890; CAA28573.1; R EMBL; X04890; CAA28573.1; R EMBL; V00290; CAA23558.1; ALT_SEQ. EMBL; M87049; AAA67571.1; ALT_SEQ. EMBL; M2000453; AAC77488.1; ALT_SEQ. EMBL; M37337; AAA24608.1; EMBL; X02413; CAA26766.1;
                                                                                                                                                                                                                                                                                                  modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 28-548 FROM N.A. STRAIN-K12 / MUTANT ILVO2096; MEDLINE-81199435; Pubmed-7015336; Lawther R.P., Calhoun D.H., Adams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Science [3]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chromosome region be Gene 97:21-27(1991).
                                                   PIR; S30666; S30666.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence.";
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                                                                L; X02413; CAA2626
L; V00289; CAA2355
; A26570; YCEC.
; JQ0875; JQ0875.
; S30665; S30665.
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99; -.
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F., Riley J., C
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"Multivalent translational control of transcription termination at attenuator of livGEDA operon of Escherichia coli K-12."; proc. Natl. Acad. Sci. U.S. A. 77:1862-1866(1980).
-I- CATALYTIC ACTIVITY: 2-ACETOLACTATE + CO(2) = 2-PYRUVATE (THIS ENZYME ALSO CATALYZES FORMATION OF 2-ACETO-2-HYDROXYBUTANOATE)
                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entrepean Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kuramitsu S., Ogawa T., Ogawa H., Kagamiyama H. "Branched-chain amino acid aminotransferase of nucleotide sequence of the ilvE gene and the de
                                                                                                                                                                                                                                                            COFACTOR: THIAMINE PYROPHOSPHATE, AND MAGNESIUM ION.
PATHMAY: FIRST STEP IN VALINE AND ISOLEUCINE BIOSYNTHESIS.
SUBUNIT: TEPTRAMER OF TWO LARGE AND TWO SMALL CHAINS.
MISCELLANEOUS: E.COLI CONTAINS GENES FOR 3 AHAS ISOZYMES: ILVBN,
MISCELLANEOUS: E.COLI CONTAINS GENES FOR 3 AHAS ISOZYMES: ILVBN,
MISCELLANEOUS: E.COLI CONTAINS GENES FOR 3 AHAS ISOZYMES: ILVBN,
MISCELLANEOUS: E.COLI CONTAINS GENES FOR 3 AHAS ISOZYMES: ILVBN,
MISCELLANEOUS: ILVGN, THE VAL-INHIBITABLE ILVBN & ILVTH ARE
EXPRESSED: ILVGN, VAL-RESISTANT, IS EXPRESSED IN STRAINS HAVING
THE ILVO MUTATION. THE ILVOZO96 MUTATION (AN INSERTION OF 2 BP)
CAUSES A FRAMESHIFT IN TRANSLATION, PERMITTING THE EXPRESSION OF
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(See http://www.isb-sib.ch/announce/
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Best Local Similarity
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033112;
30-MAY-2000
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Branched-chain amino acid biosynthesis; Flavoprotein;
Thiamine pyrophosphate; Lyase.

ACT_SITE 47 47 BY SIMILARITY.

CONFLICT 284 284 S -> F (IN REF. 2).

CONFLICT 284 284 S -> F (IN REF. 2).

SEQUENCE 548 AA; 59224 MW; A452857DA164C6DA CRC64;
Mycobacterium leprae. Bacteria; Firmicutes;
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ILVB OR MLCB637.20.
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(Rel. 39,
E SYNTHASE
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                                                                                 Corynebacterineae;
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                                                                                 Actinobacteria; Actinobacterida nebacterineae; Mycobacteriaceae;
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Last annotation update)
(EC 4.1.3.18) (ACETOHYDROXY-ACID
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Pred. No. 4.6e
91; Mismatches
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DT AC

ILVB_ARATH P17597; 01-AUG-1990 01-AUG-1990

(Rel.

Created)
Last sequence

update)

STANDARD; 15, 15,

RESULT 13 ILVB_ARATH

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the Euro
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Branched-chain amino acid biosynthesis;
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                           LAYPG-PVLIDIVTDPNA
                                                                                                                                           GSFRHGTMANALPHAIGAQSVDRNRQVIAMCGDGGLGMLLGELLTVKLHQLPLKAVVFNN
                                                                                                                                                                                                                                DPAEIGKNRHADVPIVGDVKAVIVELIAMLRHYEVPGNIEMTDWWSYLDGVRKTY----
                                                                                                                                                                                                                                                   NGAHIGRRTTVKYPVTGDVAATIENILPHVK-----EKTD-RSFLDRMLKAHERKLS
                                                                                                                                                                                                                                                                                                                    YIQHENPFEVGMSGLLGYGACVDASNEADLLILLGTDF-----PYSDFLPKDNVAQVDI
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RAINNRPVVIDFIVGADA
                                                       GNLGMVRQWQALFYQERYSQTDLATHSHRIPDFVKLAEALGCVGLRCECEEDVVDVINQA
                                                                                    SSLGMVKLEMLVEGQPEFG-TD---
                                                                                                                                                                         ----PLSYSPQSDGTLSPEYVIEKLGEIVGPEAVYVAGVGQHQMWAAQFI-SYEKPRTWL
                                                                                                                                                                                                                                                                                                                                               {\tt TKPHNRQIRAAAKLIADARKPVLYVGGGVIRGEATEQLRDLAELTGIPVVSTLMARGAFP}
                                                                                                                  NSGGLGTMGFAIPAAMGAKIARPEAEVWAIDGDGCFQMTNQELATCAIEGAPIKVALINN
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60; Conservative
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28.7%;
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Pred. No. 1e-2
97; Mismatches
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53FBA3DA76A169D1
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tions on its
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Query Match
Best Local S
Matches 158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2000 (Rel. 40, ACETOLACTATE SYNTHASE SYNTHASE) (ALS).
                                                                                                                                                                                                                                                                                                                                                                   PFAM; PF00205; TPP_enzymes; 1.
PROSITE; PS00187; TPP_ENZYMES; 1.
Branched-chain amino acid biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sathasivan K., Haughn G.W., Murai "Molecular basis of imidazolinone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sathasivan K., Haughn G.W., Murai N.;
"Nucleotide sequence of a mutant acetolactate
imidazolinone-resistant Arabidopsis thallana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-CV. COLUMBIA;
MEDLINE-90245681; PubMed-2336405;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM
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125
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BIOTECHNOLOGY: INTRODUCED BY GENETIC MANIPULATION BIOTECHNOLOGY: INTRODUCED BY GENETIC MANIPULATION SULFONYLUREA RESISTANT FLAX BY THE UNIVERSITY OF SIMILARITY: WITH OTHER ENZYMES WHICH REQUIRE TPP.
                                                                                                                                                                                                                                                                                        SITE
GYCEMVNGGEQGERILHHAIQSTMAGK-GVSVVVIPGDIAKEDAGDGTYSNSTISSGTPV
                                           AEQLIDTLEAQGVKRIYGLVGDSLNPIVDAV-RQSDIEWVHVRNEEAAAFAAGAESLITG
                                                                                                                                                                                                                                                                                                                                                                                                                                                 S09502; YCMU
                              KPGTCTATSGPGATNLVSGLADALLDSVPLVATTGQVPRRMIGTDAFQETPIVEVTRSIT
                                                                                          ADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPRHEQGGVFAAEGYARSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X51514; CAA35887.1;
                                                                                                                                                                                                                                                                                                                                      Chloroplast;
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                                                                                                                                                                                                                                                                                                                                                    chain amino acid biosynthesis; Flavoprotein; pyrophosphate; Herbicide resistance; Transit
                                                                                                                                                                                                                                                                                                                                                                                                                 IPR000399; -
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144
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72585
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27.5%;
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PRECURSOR (EC 4.1.3.18) (ACETOHYDROXY-ACID
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X
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Pred.
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BY SIMILARITY.
P -> S (IN MUTANT GH 5
S -> N (IN MUTANT CH 5
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                                                                                                                                                         Mismatches
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herbicide
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15-DEC-1998
15-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POXB_STRPN
Q54970;
                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restruce by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                              MEDLINE=96417859; PubMed=8820650;
Spellerberg B., Cundell D.R., Sandros J., Pearce
Idanpaan-Heikkila I., Rosenow C., Masure H.R.;
"Pyruvate oxidase, as a determinant of virulence
                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus pneumoniae. Bacteria; Firmicutes; Bac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRPN
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                                                                                                                                                                                              . MICTODIO1. 19:803-813(1996).
FUNCTION: IMPORTANT FOR THE AEROBIC GROWTH. DE PYRUVATE IN FOUR STEPS. THE ENERGY RELEASED IS IN ACETYL PHOSPHATE (BY SIMILARITY).
CAPALYTIC ACTIVITY: PYRUVATE + ORTHOPHOSPHATE ACETYL PHOSPHATE + CO(2) + H(2)0(2).
COFACTOR: THIAMINE PYROPHOSPHATE, FAD AND MAGN
                                                                                                                                                                   SIMILARITY: WITH OTHER ENZYMES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         998 (Rel. 37, Created)
998 (Rel. 37, Last sequence update)
998 (Rel. 37, Last annotation update)
98 (Rel. 37, Last annotation CXIDASE)
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                                                                                                                                                                                                                                                                                                                                                                                                                               Bacillus/Clostridium group; Streptococcaceae;
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                                                                 (See http://www.isb-sib.
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01-AUG-1995 (Rel. 23, I
01-OCT-1996 (Rel. 34, I
01-OCT-1976 (Rel. 34, I
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ACT_SITE
          SEQUENCE FROM N.A.
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MEDLINE-91375448; PubMed-1896019;
Rutledge R.G., Ouellet T., Hattori J.,
"Molecular characterization and geneti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oxidoreductase;
                                                                                                Brassica napus (Rape).
Eukaryota; Viridiplantae; Embryophyta;
Magnoliophyta; eudicotyledons; core eu
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rase; Flavoprotein;
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Thiamine pyrophosphate; Herbicide resistance;
Lyase; Chloroplast; Multigene family.
TRANSIT 1 82 CHLOROPLAST (BY:
CHAIN 83 655 ACETOLACTATE YN
BCT_SITE 129 BY SINILARITY.
SEQUENCE 655 AA; 71288 MW; 1BEAD7D7AODAD9:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (S or send an email to license@isb-sib.ch).
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CAPALYTIC ACTIVITY: 2-ACETOLACTATE + CO(2) = 2-PYRUVATE (THIS ENZYME ALSO CATALYZES FORMATION OF 2-ACETO-2-HYDROXY-BUTANOATE).

COFACTOR: THIAMINE PYROPHOSPHATE, AND MAGNESIUM ION.

PATHWAY: FIRST STEP IN VALIME AND ISOLEUCIME BIOSYNTHESIS.

MISCELLANEOUS: ACETOLACTATE SYNTHASE IS THE TARGET ENZYME FOR SULFONYLUREA AND IMIDASOLINONE HERBICIDES.

SIMILARITY: WITH OTHER ENZYMES WHICH REQUIRE TPP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        European
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                                                                                                                                                                                                                                                                                                                                                                                                          KHNYLVMDVDDIPRIVQEAFFLATSGRPGPVLVDVPKDI-QQQLAIPNWDQPMRLPGYMS
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149; Conserv
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                              <u>MQWEDRFYKANRAHTYLGDPARENETFPNMLQFAGACGTPAARVTKKEELREATQ</u>
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26.3%;
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